

SEQUENCE LISTING

<110> Wiley, Steven R.
Goodwin, Raymond G.

<120> Cytokine that Induces Apoptosis

<130> 2835-E

<140> 09/320,424
<141> 1999-05-26

<150> 09/190,046
<151> 1998-11-10

<150> 09/048,641
<151> 1998-03-26

<150> 08/670,354
<151> 1996-06-25

<150> 08/548,368
<151> 1995-11-01

<150> 08/496,632
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<170> PatentIn Ver. 2.0

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ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc 162
Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu
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ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag 210
Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu
30 35 40
ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc 258
Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe
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tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg 306
 Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met
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 Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg
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aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa gaa 402
 Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
 90 95 100 105

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 Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
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 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 125 130 135

tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc 546
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
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agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat 642
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 170 175 180 185

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 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
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 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 220 225 230

gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag 834
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 235 240 245

ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg 882
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ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc 930
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 35 40 45
 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
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 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 65 70 75 80
 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
 85 90 95
 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
 100 105 110
 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
 115 120 125
 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
 130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 145 150 155 160
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 165 170 175
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 180 185 190
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 195 200 205
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 210 215 220
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
 225 230 235 240
 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
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 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser
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 ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc ctg cag 158
 Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln
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 tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag ctg aag 206
 Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys
 30 35 40
 cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc tta aaa 254
 Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys
 45 50 55
 gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg aac agc 302
 Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser
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Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
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Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
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Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
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Val Ile Cys Ile Val Leu Leu Gln Val Leu Leu Gln Ala Val Ser Val
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gct gtg act tac atg tac ttc acc aac gag atg aag cag ctg cag gac 199
Ala Val Thr Tyr Met Tyr Phe Thr Asn Glu Met Lys Gln Leu Gln Asp
40 45 50

aat tac tcc aaa att gga cta gct tgc ttc tca aag acg gat gag gat 247
Asn Tyr Ser Lys Ile Gly Leu Ala Cys Phe Ser Lys Thr Asp Glu Asp
55 60 65

ttc tgg gac tcc act gat gga gag atc ttg aac aga ccc tgc ttg cag 295
Phe Trp Asp Ser Thr Asp Gly Glu Ile Leu Asn Arg Pro Cys Leu Gln
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gtt aag agg caa ctg tat cag ctc att gaa gag gtg act ttg aga acc 343
Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr Leu Arg Thr
85 90 95

ttt cag gac acc att tct aca gtt cca gaa aag cag cta agt act cct 391
Phe Gln Asp Thr Ile Ser Thr Val Pro Glu Lys Gln Leu Ser Thr Pro
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ccc ttg ccc aga ggt gga aga cct cag aaa gtg gca gct cac att act 439
Pro Leu Pro Arg Gly Gly Arg Pro Gln Lys Val Ala Ala His Ile Thr
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Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile Ser Lys Asp
135 140 145

gga aag acc tta ggc cag aag att gaa tcc tgg gag tcc tct cgg aaa 535
Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser Ser Arg Lys
150 155 160

ggg cat tca ttt ctc aac cac gtg ctc ttt agg aat gga gag ctg gtc 583
Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly Glu Leu Val
165 170 175

atc gag cag gag ggc ctg tat tac atc tat tcc caa aca tac ttc cga 631
Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
180 185 190 195

ttt cag gaa gct gaa gac gct tcc aag atg gtc tca aag gac aag gtg 679
Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys Asp Lys Val
200 205 210

aga acc aaa cag ctg gtg cag tac atc tac aag tac acc agc tat cgg 727
Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
215 220 225

gat ccc ata gtg ctc atg aag agc gcc aga aac agc tgt tgg tcc aga 775
Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Arg
230 235 240

gat gcc gag tac gga ctg tac tcc atc tat cag gga gga ttg ttc gag 823
Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Leu Phe Glu
245 250 255

cta aaa aaa aat gac agg att ttt gtt tct gtg aca aat gaa cat ttg 871
Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
260 265 270 275

atg gac ctg gat caa gaa gcc agc ttc ttt gga gcc ttt tta att aac 919
Met Asp Leu Asp Gln Glu Ala Ser Phe Phe Gly Ala Phe Leu Ile Asn
280 285 290

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gcattgcctgg aaagcgactg aactgggttag gatattggcct ggctgtagaa acctcaggac 1039

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 Leu Gln Asp Asn Tyr Ser Lys Ile Gly Leu Ala Cys Phe Ser Lys Thr
 50 55 60
 Asp Glu Asp Phe Trp Asp Ser Thr Asp Gly Glu Ile Leu Asn Arg Pro
 65 70 75 80
 Cys Leu Gln Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr
 85 90 95
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 100 105 110
 Ser Thr Pro Pro Leu Pro Arg Gly Arg Pro Gln Lys Val Ala Ala
 115 120 125
 His Ile Thr Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile
 130 135 140
 Ser Lys Asp Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser
 145 150 155 160
 Ser Arg Lys Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly
 165 170 175
 Glu Leu Val Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr
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 Tyr Phe Arg Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys
 195 200 205
 Asp Lys Val Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr
 210 215 220
 Ser Tyr Pro Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys
 225 230 235 240
 Trp Ser Arg Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
 245 250 255
 Leu Phe Glu Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn
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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met	
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Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His	
35 40 45	
ata gag aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act	192
Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr	
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aga tct acc tct gag gaa acc att tct aca gtt caa gaa aag caa caa	240
Arg Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln	
65 70 75 80	
aat att tct ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct	288
Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala	
85 90 95	
cac ata act ggg acc aga gga aga agc aac aca ttg tct tct cca aac	336
His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn	
100 105 110	
tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca	384
Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser	
115 120 125	
tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt	432
Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly	
130 135 140	
gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca	480
Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr	
145 150 155 160	
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Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys	
165 170 175	
caa atg gtc caa tat att tac aaa tac aca agt tat cct gac cct ata	576
Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile	
180 185 190	
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Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu	
195 200 205	
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Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu	
210 215 220	
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Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met	
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 35 40 45
 Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
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 Arg Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln
 65 70 75 80
 Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
 85 90 95
 His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
 100 105 110
 Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
 115 120 125
 Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
 130 135 140
 Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
 145 150 155 160
 Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
 165 170 175
 Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
 180 185 190
 Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
 195 200 205
 Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
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 Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser Ser
 20 25 30
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 Asp Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
 35 40 45
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 Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
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 Glu Arg Thr Arg Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
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 Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
 85 90 95
 gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg tct 336
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 100 105 110
 tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc 384
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 115 120 125
 tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg 432
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 130 135 140
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 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 145 150 155 160
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 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 165 170 175
 aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct 576
 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 180 185 190

gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa 624
 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 195 200 205

gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag 672
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 210 215 220

ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg 720
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 225 230 235 240

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Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
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 65 70 75 80

Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
 85 90 95

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 100 105 110

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 115 120 125

Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 130 135 140

Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 145 150 155 160

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 165 170 175

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 180 185 190

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
195 200 205

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
210 215 220

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
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<400> 14

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Ala Leu Gln Gly Gln
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Val Gln His Leu Gln Ala Ala Phe Ser Gln Tyr
20 25

<210> 15

<211> 34

<212> PRT

<213> LZ peptide

<400> 15

Asp Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys
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Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly
20 25 30

Glu Arg

<210> 16

<211> 28

<212> PRT

<213> LZ peptide

<400> 16

Ser Leu Ala Ser Leu Arg Gln Gln Leu Glu Ala Leu Gln Gly Gln Leu
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Gln His Leu Gln Ala Ala Leu Ser Gln Leu Gly Glu
20 25

<210> 17

<211> 28

<212> PRT

<213> LZ peptide

<400> 17
 Ser Ile Ala Ser Ile Arg Gln Gln Ile Glu Ala Ile Gln Gly Gln Ile
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Gln His Ile Gln Ala Ala Ile Ser Gln Ile Gly Glu
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<210> 18
 <211> 77
 <212> DNA
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<400> 18
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 ttcaagaggg cagtgc 77

<210> 19
 <211> 26
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 <213> GH Leader

<400> 19
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 1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
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<210> 20
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: artificial
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<400> 20
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<210> 21
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<220>
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<400> 21
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1 5

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<400> 24
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1 5

<210> 25
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<400> 25
Met Gly Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20